RAW SEQUENCE LISTING ERROR REPORT

BIOTECHNOLOGY SYSTEMS BRANCH
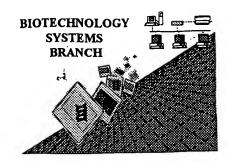
The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: __09/758,019__

Source: __OIPE__

Date Processed by STIC: __8/17/2001__

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).
Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: *09/758,017*

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics
Wrapped Aminos

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

· 2 _____ Invalid Line Length

The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 _____ Misaligned Amino
Numbering

The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 _____ Non-ASCII

The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 _____ Variable Length

Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 _____ PatentIn 2.0
"bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 _____ Skipped Sequences
(OLD RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 _____ Skipped Sequences
(NEW RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 _____ Use of n's or Xaa's
(NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.

10 _____ Invalid <213>
Response

Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11 _____ Use of <220>

Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12 _____ PatentIn 2.0
"bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 _____ Misuse of n

n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

AMC/MH – Biotechnology Systems Branch – 08/21/2001

OIPE

Does Not Comply
Corrected Diskette Needed

```
  3 <110> APPLICANT: Lanes, Olav
  4         Willasen, Nils Peder
  5         Guddal, Per Henrik
  6         Gjellesvik, Dag Rune
  8 <120> TITLE OF INVENTION: Cod uracil-DNA glycosylase, gene coding therefore,
  9         recombinant DNA containing said gene or operative parts
 10         thereof, a method for preparing said protein and the
 11         use of said protein or said operative pa
 13 <130> FILE REFERENCE: U013209-3
 15 <140> CURRENT APPLICATION NUMBER: 09/758,017
 16 <141> CURRENT FILING DATE: 2001-01-10
 18 <150> PRIOR APPLICATION NUMBER: 2000 5428
 19 <151> PRIOR FILING DATE: 2000-10-27
 21 <150> PRIOR APPLICATION NUMBER: 2000 0163
 22 <151> PRIOR FILING DATE: 2000-01-12
 24 <160> NUMBER OF SEQ ID NOS: 19
 26 <170> SOFTWARE: PatentIn Ver. 2.0
```

ERRORED SEQUENCES

```
131 <210> SEQ ID NO: 2
132 <211> LENGTH: 301
133 <212> TYPE: PRT
134 <213> ORGANISM: Gadus morhua
136 <400> SEQUENCE: 2
137 Met Leu Phe Lys Leu Gly Leu Cys Gln Arg Cys Ile Ser Ser Asn Arg
138      1               5                  10                  15
140 Xaa Leu Pro Gly Leu Leu Ile Pro Gln Thr Leu Cys Phe Ser Lys Leu
141              20                  25                  30
143 Met Lys Ile Thr Pro Lys Lys Leu Arg Ser Ser Asn Val Glu Gln Lys
144              35                  40                  45
146 Thr Ser Ser Pro Gln Leu Ser Val Glu Gln Leu Glu Arg Met Ala Lys
147          50                  55                  60
149 Asn Lys Lys Ala Ala Leu Asp Lys Ile Arg Ala Lys Ala Thr Pro Ala
150      65                  70                  75                  80
152 Gly Phe Gly Glu Thr Trp Arg Arg Glu Leu Ala Ala Glu Phe Glu Lys
153              85                  90                  95
155 Pro Tyr Phe Lys Gln Leu Met Ser Phe Val Ala Asp Glu Arg Ser Arg
156              100                 105                 110
158 His Thr Val Tyr Pro Pro Ala Asp Gln Val Tyr Ser Ser Thr Glu Met
159          115                 120                 125
161 Cys Asp Ile Gln Asp Val Lys Val Val Ile Leu Gly Gln Asp Pro Tyr
162          130                 135                 140
164 His Gly Pro Asn Gln Ala His Gly Leu Cys Phe Ser Val Gln Lys Pro
165 145                 150                 155                 160
167 Val Pro Pro Pro Pro Ser Leu Val Asn Ile Tyr Lys Glu Leu Cys Thr
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E--> (marking at line 140)

RAW SEQUENCE LISTING   DATE: 08/17/2001
PATENT APPLICATION: US/09/758,017   TIME: 12:01:31

Input Set : A:\U0132093.app
Output Set: N:\CRF3\08162001\I758017.raw

```
168                  165                  170                  175
170 Asp Ile Asp Gly Phe Lys His Pro Gly His Gly Asp Leu Ser Gly Trp
171              180                  185                  190
173 Ala Lys Gln Gly Val Leu Leu Leu Asn Ala Val Leu Thr Val Arg Ala
174         195                  200                  205
176 His Gln Ala Asn Ser His Lys Asp Arg Gly Trp Glu Thr Phe Thr Asp
177     210                  215                  220
179 Ala Val Ile Lys Trp Leu Ser Val Asn Arg Glu Gly Val Val Phe Leu
180 225                  230                  235                  240
182 Leu Trp Gly Ser Tyr Ala His Lys Lys Gly Ala Thr Ile Asp Arg Lys
183              245                  250             .        255
185 Arg His His Val Leu Gln Ala Val His Pro Ser Pro Leu Ser Ala His
186         .        260                  265   .              270
188 Arg Gly Phe Leu Gly Cys Lys His Phe Ser Lys Ala Asn Gly Leu Leu
189         275                  280                  285
191 Lys Leu Ser Gly Thr Glu Pro Ile Asn Trp Arg Ala Leu
192     290              .        295                  300
```

Use of n and/or Xaa has been detected in the Sequence Listing.
Review the Sequence Listing to insure a corresponding
explanation is presented in the.<220> to <223> fields of
each sequence using n or Xaa.

VERIFICATION SUMMARY DATE: 08/17/2001
PATENT APPLICATION: **US/09/758,017** TIME: 12:01:32

Input Set : **A:\U0132093.app**
Output Set: **N:\CRF3\08162001\I758017.raw**

L:43 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:1
L:43 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:140 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:2